

PCT09

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/762,258

DATE: 02/13/2001
TIME: 15:01:20

Input Set : A:\Lu5002us.txt
Output Set: N:\CRF3\02132001\I762258.raw

ENTERED

3 <110> APPLICANT: Gout, Ivan
 4 Hara, Kenta
 5 Waterfield, Michael
 6 Yonezawa, Kazu
 7 Ludwig Institute for Cancer Research
 9 <120> TITLE OF INVENTION: Identification and Functional Characterization of a
 10 Novel Ribosomal S6 Protein Kinase
 12 <130> FILE REFERENCE: 40750-5002-US
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/762,258
 C--> 15 <141> CURRENT FILING DATE: 2001-02-05
 17 <150> PRIOR APPLICATION NUMBER: PCT/US99/17595
 18 <151> PRIOR FILING DATE: 1999-08-04
 20 <150> PRIOR APPLICATION NUMBER: 60/095,268
 21 <151> PRIOR FILING DATE: 1998-08-04
 23 <160> NUMBER OF SEQ ID NOS: 8
 25 <170> SOFTWARE: PatentIn Ver. 2.0
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 1816
 29 <212> TYPE: DNA
 30 <213> ORGANISM: Homo sapiens
 32 <220> FEATURE:
 33 <221> NAME/KEY: CDS
 34 <222> LOCATION: (77)..(1561)
 35 <223> OTHER INFORMATION: p70(beta) S6 Kinase gene
 37 <400> SEQUENCE: 1
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 42 1 5 10
 44 gcc atg gcg gcc gtg ttt gat ttg gat ttg gag acg gag gaa ggc agc 160
 45 Ala Met Ala Ala Val Phe Asp Leu Asp Leu Glu Thr Glu Gly Ser
 46 15 20 25
 48 gag ggc gag ggc gag cca gag ctc agc ccc gcg gac gca tgt ccc ctt 208
 49 Glu Gly Glu Gly Glu Pro Glu Leu Ser Pro Ala Asp Ala Cys Pro Leu
 50 30 35 40
 52 gcc gag ttg agg gca gct ggc cta gag cct gtg gga cac tat gaa gag 256
 53 Ala Glu Leu Arg Ala Ala Gly Leu Glu Pro Val Gly His Tyr Glu Glu
 54 45 50 55 60
 56 gtg gag ctg act gag acc agc gtg aac gtt ggc cca gag cgc atc ggg 304
 57 Val Glu Leu Thr Ser Val Asn Val Gly Pro Glu Arg Ile Gly
 58 65 70 75
 60 ccc cac tgc ttt gag ctg ctg cgt gtg ctg ggc aag ggg ggc tat ggc 352
 61 Pro His Cys Phe Glu Leu Leu Arg Val Leu Gly Lys Gly Tyr Gly
 62 80 85 90
 64 aag gtg ttc cag gtg cga aag gtg caa ggc acc aac ttg ggc aaa ata 400
 65 Lys Val Phe Gln Val Arg Lys Val Gln Gly Thr Asn Leu Gly Lys Ile
 66 95 100 105

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69	Tyr	Ala	Met	Lys	Val	Leu	Arg	Lys	Ala	Lys	Ile	Val	Arg	Asn	Ala	Lys	
70	110				115						120						
72	gac	aca	gca	cac	aca	cgg	gct	gag	cg	aac	att	cta	gag	tca	gtg	aag	496
73	Asp	Thr	Ala	His	Thr	Arg	Ala	Glu	Arg	Asn	Ile	Leu	Glu	Ser	Val	Lys	
74	125				130						135					140	
76	cac	ccc	ttt	att	gtg	gaa	ctg	gcc	tcc	cag	act	ggt	ggc	aaa		544	
77	His	Pro	Phe	Ile	Val	Glu	Leu	Ala	Tyr	Ala	Phe	Gln	Thr	Gly	Gly	Lys	
78					145					150					155		
80	ctc	tac	ctc	atc	ctt	gag	tgc	ctc	agt	ggt	ggc	gag	ctc	tcc	acg	cat	592
81	Leu	Tyr	Leu	Ile	Leu	Glu	Cys	Leu	Ser	Gly	Gly	Glu	Leu	Phe	Thr	His	
82					160				165			170					
84	ctg	gag	cga	gag	ggc	atc	tcc	ctg	gaa	gat	acg	gcc	tgc	tcc	tac	ctg	640
85	Leu	Glu	Arg	Glu	Gly	Ile	Phe	Leu	Glu	Asp	Thr	Ala	Cys	Phe	Tyr	Leu	
86					175				180			185					
88	gct	gag	atc	acg	ctg	gcc	ctg	ggc	cat	ctc	cac	tcc	cag	ggc	atc	atc	688
89	Ala	Glu	Ile	Thr	Leu	Ala	Leu	Gly	His	Leu	His	Ser	Gln	Gly	Ile	Ile	
90					190				195			200					
92	tac	cg	gac	ctc	aag	ccc	gag	aac	atc	atg	ctc	agc	agc	cag	ggc	cac	736
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96	atc	aaa	ctg	acc	gac	ttt	gga	ctc	tgc	aag	gag	tct	atc	cat	gag	ggc	784
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102					240				245			250					
104	att	ctg	gtg	cgc	agt	ggc	cac	aac	cgg	gct	gtg	gac	tgg	tgg	agc	ctg	880
105	Ile	Leu	Val	Arg	Ser	Gly	His	Asn	Arg	Ala	Val	Asp	Trp	Trp	Ser	Leu	
106					255				260			265					
108	ggg	gcc	ctg	atg	tac	gac	atg	ctc	act	gga	tgc	ccg	ccc	ttt	acc	gca	928
109	Gly	Ala	Leu	Met	Tyr	Asp	Met	Leu	Thr	Gly	Ser	Pro	Pro	Phe	Thr	Ala	
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112	gag	aa	c	gg	aa	aa	cc	at	g	at	ac	tc	gg	aa	ct	g	976
113	Glu	Asn	Arg	Lys	Lys	Thr	Met	Asp	Lys	Ile	Ile	Arg	Gly	Lys	Leu	Ala	
114					285				290			295				300	
116	ctg	ccc	ccc	tac	ctc	acc	cca	gat	gcc	cg	gac	ctt	gtc	aaa	aag	ttt	1024
117	Leu	Pro	Pro	Tyr	Leu	Thr	Pro	Asp	Ala	Arg	Asp	Leu	Val	Lys	Lys	Phe	
118					305				310			315					
120	ctg	aaa	cg	aa	at	cc	ag	at	gg	gg	gt	gg	cc	gg	gat	gct	1072
121	Leu	Lys	Arg	Asn	Pro	Ser	Gln	Arg	Ile	Gly	Gly	Pro	Gly	Asp	Ala		
122					320				325			330					
124	gct	gat	gtg	cag	aga	cat	ccc	ttt	tcc	cg	cac	atg	aat	tgg	gac	gac	1120
125	Ala	Asp	Val	Gln	Arg	His	Pro	Phe	Phe	Arg	His	Met	Asn	Trp	Asp	Asp	
126					335				340			345					
128	ctt	ctg	gcc	tgg	cgt	gtg	gac	ccc	cct	tcc	agg	ccc	tgt	ctg	cag	tca	1168
129	Leu	Leu	Ala	Trp	Arg	Val	Asp	Pro	Pro	Phe	Arg	Pro	Cys	Leu	Gln	Ser	
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132	gag	gag	gac	gtg	agc	cag	ttt	gat	acc	cgc	ttc	aca	cg	cag	acg	ccg	1216

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137	Val	Asp	Ser	Pro	Asp	Asp	Asp	Thr	Ala	Leu	Ser	Glu	Ser	Ala	Asn	Gln	Ala
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140	ttc	ctg	ggc	ttc	aca	tac	gtg	gcg	ccg	tct	gtc	ctg	gac	agc	atc	aag	1312
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144	gag	ggc	ttc	tcc	ttc	cag	ccc	aag	ctg	cgc	tca	ccc	agg	cgc	ctc	aac	1360
145	Glu	Gly	Phe	Ser	Phe	Gln	Pro	Lys	Leu	Arg	Ser	Pro	Arg	Arg	Leu	Asn	
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148	agt	agc	ccc	cgg	gtc	ccc	gtc	agc	ccc	ctc	aag	ttc	tcc	cct	ttt	gag	1408
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152	ggg	ttt	cgg	ccc	agc	ccc	agc	ctg	ccg	gag	ccc	acg	gag	cta	cct	cta	1456
153	Gly	Phe	Arg	Pro	Ser	Pro	Ser	Leu	Pro	Glu	Pro	Thr	Glu	Leu	Pro	Leu	
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156	cct	cca	ctc	ctg	cca	ccg	ccg	ccc	tcg	acc	acc	gcc	cct	ctc	ccc		1504
157	Pro	Pro	Leu	Leu	Pro	Pro	Pro	Pro	Pro	Ser	Thr	Thr	Ala	Pro	Leu	Pro	
158							465		470						475		
160	atc	cgt	ccc	ccc	tca	ggg	acc	aag	tcc	aag	agg	ggc	cgt	ggg	cgt		1552
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 207 Val Leu Arg Lys Ala Lys Ile Val Arg Asn Ala Lys Asp Thr Ala His
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 211 130 135 140
 213 Val Glu Leu Ala Tyr Ala Phe Gln Thr Gly Gly Lys Leu Tyr Leu Ile
 214 145 150 155 160
 216 Leu Glu Cys Leu Ser Gly Gly Glu Leu Phe Thr His Leu Glu Arg Glu
 217 165 170 175
 219 Gly Ile Phe Leu Glu Asp Thr Ala Cys Phe Tyr Leu Ala Glu Ile Thr
 220 180 185 190
 222 Leu Ala Leu Gly His Leu His Ser Gln Gly Ile Ile Tyr Arg Asp Leu
 223 195 200 205
 225 Lys Pro Glu Asn Ile Met Leu Ser Ser Gln Gly His Ile Lys Leu Thr
 226 210 215 220
 228 Asp Phe Gly Leu Cys Lys Glu Ser Ile His Glu Gly Ala Val Thr His
 229 225 230 235 240
 231 Thr Phe Cys Gly Thr Ile Glu Tyr Met Ala Pro Glu Ile Leu Val Arg
 232 245 250 255
 234 Ser Gly His Asn Arg Ala Val Asp Trp Trp Ser Leu Gly Ala Leu Met
 235 260 265 270
 237 Tyr Asp Met Leu Thr Gly Ser Pro Pro Phe Thr Ala Glu Asn Arg Lys
 238 275 280 285
 240 Lys Thr Met Asp Lys Ile Ile Arg Gly Lys Leu Ala Leu Pro Pro Tyr
 241 290 295 300
 243 Leu Thr Pro Asp Ala Arg Asp Leu Val Lys Lys Phe Leu Lys Arg Asn
 244 305 310 315 320
 246 Pro Ser Gln Arg Ile Gly Gly Pro Gly Asp Ala Ala Asp Val Gln
 247 325 330 335
 249 Arg His Pro Phe Phe Arg His Met Asn Trp Asp Asp Leu Leu Ala Trp
 250 340 345 350
 252 Arg Val Asp Pro Pro Phe Arg Pro Cys Leu Gln Ser Glu Glu Asp Val
 253 355 360 365
 255 Ser Gln Phe Asp Thr Arg Phe Thr Arg Gln Thr Pro Val Asp Ser Pro
 256 370 375 380
 258 Asp Asp Thr Ala Leu Ser Glu Ser Ala Asn Gln Ala Phe Leu Gly Phe
 259 385 390 395 400
 261 Thr Tyr Val Ala Pro Ser Val Leu Asp Ser Ile Lys Glu Gly Phe Ser
 262 405 410 415
 264 Phe Gln Pro Lys Leu Arg Ser Pro Arg Arg Leu Asn Ser Ser Pro Arg
 265 420 425 430
 267 Val Pro Val Ser Pro Leu Lys Phe Ser Pro Phe Glu Gly Phe Arg Pro
 268 435 440 445
 270 Ser Pro Ser Leu Pro Glu Pro Thr Glu Leu Pro Leu Pro Pro Leu Leu
 271 450 455 460
 273 Pro Pro Pro Pro Ser Thr Thr Ala Pro Leu Pro Ile Arg Pro Pro
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 293 1 5
 294 ttt tac cca gcc ccg gac ttc cga gac agg gaa gct gag gac atg gca 102
 295 Phe Tyr Pro Ala Pro Asp Phe Arg Asp Arg Glu Ala Glu Asp Met Ala 25
 296 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200
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 298 gga gtg ttt gac ata gac ctg gac cag cca gag gac gcg ggc tct gag 150
 299 Gly Val Phe Asp Ile Asp Leu Asp Gln Pro Glu Asp Ala Gly Ser Glu 150
 300 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200
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 303 Asp Glu Leu Glu Gly Gly Gln Leu Asn Glu Ser Met Asp His Gly 198
 304 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200
 305 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200
 306 gga gtt gga cca tat gaa ctt ggc atg gaa cat tgt gag aaa ttt gaa 246
 307 Gly Val Gly Pro Tyr Glu Leu Gly Met Glu His Cys Glu Lys Phe Glu 246
 308 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200
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 310 atc tca gaa act agt gtg aac aga ggg cca gaa aaa atc aga cca gaa 294
 311 Ile Ser Glu Thr Ser Val Asn Arg Gly Pro Glu Lys Ile Arg Pro Glu 294
 312 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200
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 315 Cys Phe Glu Leu Leu Arg Val Leu Gly Lys Gly Gly Tyr Gly Lys Val 342
 316 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200
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 320 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200
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 322 atg aag gtg ctt aaa aag gca atg ata gta aga aat gct aaa gat aca 438
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 324 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200
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 328 140 145 150 155 160 165 170 175 180 185 190 195 200
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 331 Phe Ile Val Asp Leu Ile Tyr Ala Phe Gln Thr Gly Lys Leu Tyr 534
 332 155 160 165 170 175 180 185 190 195 200
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 334 ctc atc ctt gag tat ctc agt gga gga aca ctt ttt atg cag tta gaa 582
 335 Leu Ile Leu Glu Tyr Leu Ser Gly Gly Glu Leu Phe Met Gln Leu Glu 582
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 338 aga gag gga ata ttt atg gaa gac act gcc tgc ttt tac ttg gca gaa 630
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L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date